AMENDMENTS

Please amend the above-identified application as follows:

In the Specification:

Please replace the paragraph beginning at page 2, line 25, with the following rewritten paragraphs:

B1

Figure 1 depicts a flow chart for array-based detection of gene expression.

Figure 2 depicts a flow chart for array-based detection of RNA alternative splicing.

Figure 3 depicts genome-wide expression profiling using oligo-ligation strategy.

Figure 4 depicts genome-wide RNA alternative splicing monitoring using oligo-ligation strategy.

Figure 5 depicts direct genotyping using a whole-genome oligo-ligation strategy.

Figure 6 depicts whole-genome oligo-ligation strategy.–

Please replace the paragraph beginning at page 2, line 26, with the following rewritten paragraph:

B2

Figure 7 depicts a preferred embodiment of the invention utilizing a poly(A)-poly(T) capture to remove unhybridized probes and targets. Target sequence 5 comprising a poly(A) sequence 6 is hybridized to target probe 115 comprising a target specific sequence 70, an adapter sequence 20, an upstream universal priming site 25, an optional label 30, and a downstream universal priming site 26. The resulting hybridization complex is contacted with a bead 51 comprising a linker 55 and a poly(T) capture probe 61.–

Please replace the paragraph beginning at page 3, line 22, with the following rewritten paragraph:

B3

Figure 10 depicts a preferred embodiment of the invention, a rolling circle embodiment utilizing a single target probe. Target 5 is hybridized to a target probe 115 comprising a first target specific sequence 15, detection position 10, an adapter sequence 20, a RCA priming site (which may be an upstream universal priming site) 140, optional label sequence 150 and a second target specific sequence 16. Following ligation, denaturation, and the addition of the RCA primer and extension by a polymerase, amplicons are generated. An optional restriction endonuclease site is not shown.–

In the Claims: